

RAW SEQUENCE LISTING

DATE: 10/01/2001

PATENT APPLICATION: US/09/617,923

TIME: 12:12:46

Input Set : N:\Crf3\RULE60\09617923.txt

Output Set: N:\CRF3\10012001\I617923.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Glimcher, Laurie H.

7 Hodge, Martin R.

9 (ii) TITLE OF INVENTION: NF-AT-INTERACTING PROTEIN NIP45 AND METHODS

10 OF USE THEREFOR

12 (iii) NUMBER OF SEQUENCES: 2

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: LAHIVE & COCKFIELD

16 (B) STREET: 60 State Street, suite 510

17 (C) CITY: Boston

18 (D) STATE: Massachusetts

19 (E) COUNTRY: USA

20 (F) ZIP: 02109-1875

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/617,923

C--> 30 (B) FILING DATE: 17-Jul-2000

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/755,584

35 (B) FILING DATE: 25-NOV-1996

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: Giulio A. DeConti, Jr.

39 (B) REGISTRATION NUMBER: 31,503

40 (C) REFERENCE/DOCKET NUMBER: HUI-026

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (617)227-7400

44 (B) TELEFAX: (617)227-5941

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1946 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

57 (ix) FEATURE:

58 (A) NAME/KEY: CDS

59 (B) LOCATION: 13..1248

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

64 ACAGTGTGGG AG ATG GCG GAA CCA CTG AGG GGA CGT GGT CCG AGG TCC

65 Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser

66

1

5

10

ENTERED

48

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68	CGC GGT GGC CGA GGC GCT CGG AGA GCC CGA GGC GCC CGT GGC CGG TGT	96
69	Arg Gly Gly Arg Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys	
70	15 20 25	
72	CCT CGC GCC CGG CAG TCT CCG GCT AGG CTC ATT CCA GAC ACC GTG CTT	144
73	Pro Arg Ala Arg Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu	
74	30 35 40	
76	GTG GAC TTG GTC AGT GAC AGC GAC GAA GAG GTC TTG GAA GTC GCA GAC	192
77	Val Asp Leu Val Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp	
78	45 50 55 60	
80	CCA GTA GAG GTG CCG GTC GCC CGC CTC CCC GCG CCG GCT AAA CCT GAG	240
81	Pro Val Glu Val Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu	
82	65 70 75	
84	CAG GAC AGC GAC AGT GAC AGT GAA GGG GCG GCC GAG GGG CCT GCG GGA	288
85	Gln Asp Ser Asp Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly	
86	80 85 90	
88	GCC CCG CGT ACA TTG GTG CGA CGG CGG CGG CGG CTG CTG GAT CCC	336
89	Ala Pro Arg Thr Leu Val Arg Arg Arg Arg Arg Leu Leu Asp Pro	
90	95 100 105	
92	GGA GAG GCG CCG GTG GTC CCA GTG TAC TCC GGG AAG GTA CAG AGC AGC	384
93	Gly Glu Ala Pro Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser	
94	110 115 120	
96	CTC AAC CTC ATT CCA GAT AAT TCA TCC CTC TTG AAA CTG TGC CCT TCA	432
97	Leu Asn Leu Ile Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser	
98	125 130 135 140	
100	GAG CCT GAA GAT GAG GCA GAT CTG ACA AAT TCT GGC AGT TCT CCC TCT	480
101	Glu Pro Glu Asp Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser	
102	145 150 155	
104	GAG GAT GAT GCC CTG CCT TCA GGT TCT CCC TGG AGA AAG AAG CTC AGA	528
105	Glu Asp Asp Ala Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg	
106	160 165 170	
108	AAG AAG TGT GAG AAA GAA GAA AAG AAA ATG GAA GAG TTT CCG GAC CAG	576
109	Lys Lys Cys Glu Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln	
110	175 180 185	
112	GAC ATC TCT CCT TTG CCC CAA CCT TCG TCA AGG AAC AAA AGC AGA AAG	624
113	Asp Ile Ser Pro Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys	
114	190 195 200	
116	CAT ACG GAG GCG CTC CAG AAG CTA AGG GAA GTG AAC AAG CGT CTC CAA	672
117	His Thr Glu Ala Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln	
118	205 210 215 220	
120	GAT CTC CGC TCC TGC CTG AGC CCC AAG CAG CAC CAG AGT CCA GCC CTT	720
121	Asp Leu Arg Ser Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu	
122	225 230 235	
124	CAG AGC ACA GAT GAT GAG GTG GTC CTA GTG GAA GGG CCT GTC TTG CCA	768
125	Gln Ser Thr Asp Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro	
126	240 245 250	
128	CAG AGC TCT CGA CTC TTT ACA CTC AAG ATC CGG TGC CGG GCT GAC CTA	816
129	Gln Ser Ser Arg Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu	
130	255 260 265	
132	GTG AGA CTG CCT GTC AGG ATG TCG GAG CCC CTT CAG AAT GTG GTG GAT	864

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133 Val Arg Leu Pro Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp
134      270                      275                      280
136 CAC ATG GCC AAT CAT CTT GGG GTG TCT CCA AAC AGG ATT CTT TTG CTT      912
137 His Met Ala Asn His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu
138 285                      290                      295                      300
140 TTT GGA GAG AGT GAA CTG TCT CCT ACT GCC ACC CCT AGT ACC CTA AAG      960
141 Phe Gly Glu Ser Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys
142                      305                      310                      315
144 CTT GGA GTG GCT GAC ATC ATT GAT TGT GTG GTG CTA GCA AGC TCT TCA      1008
145 Leu Gly Val Ala Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser
146                      320                      325                      330
148 GAG GCC ACA GAG ACA TCC CAG GAG CTC CGG CTC CGG GTG CAG GGG AAG      1056
149 Glu Ala Thr Glu Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys
150                      335                      340                      345
152 GAG AAA CAC CAG ATG TTG GAG ATC TCA CTG TCT CCT GAT TCT CCT CTT      1104
153 Glu Lys His Gln Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu
154                      350                      355                      360
156 AAG GTT CTC ATG TCA CAC TAT GAG GAA GCC ATG GGA CTC TCT GGA CAC      1152
157 Lys Val Leu Met Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His
158 365                      370                      375                      380
160 AAG CTC TCC TTC TTC TTT GAT GGG ACA AAG CTT TCA GGC AAG GAG CTG      1200
161 Lys Leu Ser Phe Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu
162                      385                      390                      395
164 CCA GCT GAT CTG GGC CTG GAA TCC GGA GAT CTC ATC GAA GTC TGG GGC      1248
165 Pro Ala Asp Leu Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
166                      400                      405                      410
168 TGAAGCTCTC ACCCTGTTTCG GACGCAAAGC CAAGACATGG AGACAATAGC TCCCAATTTT      1308
170 ATTATTGTGA TTTTTCGCCC CATAAGGGCT AACAGAAACT GAATTAGAAC TTGTTTACTT      1368
172 ATTTATTTCT GGTGCTGGGG ATTGAACCCC AGACTATGCA CATGCTAAGG ATGTATGAAG      1428
174 TGGAGGCAAA ACCAAGGCAT TACCTTTAGC CAGCCTCTAG TAGACTGTAG TGTC AAGCAA      1488
176 GTGGCTACTT GGTAGTTGTG TGGCTCTGTG TATGTTTGTG CTGTATTTGG CAGCCCCTGG      1548
178 GGCACATAGA AGGGACCTTG GCTTCCCTAC CATTTCACGT TCGCTGGTGC CCTTTCCTTC      1608
180 ATCAGATGAC TTCTGTGAAG CTGCCTATGT TGAGTGTGTT GAACTAAATG AGCTCTGCTT      1668
182 TGGGTGTCCA GGCCTGGGGT TTGTGCCGCA GTTGGAGCCA GCAGTGACTT CACTCTGACT      1728
184 TGGGACTGAG AATGCATTTT CTGGTGGAGA CACTCGGGTG CAGAAATATA ACAGAAGGTG      1788
186 ACATACATGC TGAAGCTGAG GACTAGGTCG AAAGTTAACG ACGTTGCATT TTCAGCCTTG      1848
188 GGTATCCTCT CTGCCTGCCA GGACTCTAGC CAGTGTCTGG TACACACTTC TTGGCATGGA      1908
190 CACCTAGGTC GACGCGGGCG CGATTGCGCC GACTCGAG      1946
193 (2) INFORMATION FOR SEQ ID NO: 2:
195     (i) SEQUENCE CHARACTERISTICS:
196         (A) LENGTH: 412 amino acids
197         (B) TYPE: amino acid
198         (D) TOPOLOGY: linear
200     (ii) MOLECULE TYPE: protein
202     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
204 Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser Arg Gly Gly Arg
205  1      5      10      15
207 Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys Pro Arg Ala Arg
208      20      25      30

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```

210 Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu Val Asp Leu Val
211      35      40      45
213 Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp Pro Val Glu Val
214      50      55      60
216 Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu Gln Asp Ser Asp
217      65      70      75      80
219 Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly Ala Pro Arg Thr
220      85      90      95
222 Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro Gly Glu Ala Pro
223      100     105     110
225 Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser Leu Asn Leu Ile
226      115     120     125
228 Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser Glu Pro Glu Asp
229      130     135     140
231 Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser Glu Asp Asp Ala
232 145      150     155     160
234 Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg Lys Lys Cys Glu
235      165     170     175
237 Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln Asp Ile Ser Pro
238      180     185     190
240 Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys His Thr Glu Ala
241      195     200     205
243 Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln Asp Leu Arg Ser
244      210     215     220
246 Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu Gln Ser Thr Asp
247 225      230     235     240
249 Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro Gln Ser Ser Arg
250      245     250     255
252 Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu Val Arg Leu Pro
253      260     265     270
255 Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp His Met Ala Asn
256      275     280     285
258 His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu Phe Gly Glu Ser
259      290     295     300
261 Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys Leu Gly Val Ala
262 305      310     315     320
264 Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser Glu Ala Thr Glu
265      325     330     335
267 Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys Glu Lys His Gln
268      340     345     350
270 Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu Lys Val Leu Met
271      355     360     365
273 Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His Lys Leu Ser Phe
274      370     375     380
276 Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu Pro Ala Asp Leu
277 385      390     395     400
279 Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly
280      405     410

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VERIFICATION SUMMARY

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]